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OM protein - protein search, using sw model

Tanuary 16, 2003, 16,39-12, Search time 18,9429 Seconds (without alignments) 28-464 Million cell updates/see Pun on:

Title: US-09-856-070-19
Perfect score: 65
Sequence: 1 KEELMLRLQDYEE 13 Sequence: Scoring table: BLOSUM62 Gapop 10 0 . Gapext 0.5

112892 seqs, 41475328 residues Searched.

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_40:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

		,c				
Result		Query				
O <b>X</b>	Score	Match	Match Length	ΞĤ	CII	Description
-	65	100 0	580	_	FZR1_BOVIN	P31976 bos taurus
ci	59	100.0		- 4	EZRI HUMAN	J. J. M.
m	62	156	En C		E2RI_MOUSE	-
4	44	67.7		-	RA50_SULAC	3 t T T
5	43	66.2		,-	BHS2_BRARE	Q98sp7 brachydanio
9	41	63 1	365	_	POTP1_SCHPO	
7	40	61.5		_	MOES_HUMAN	
œ	<b>.4</b>			-	MOES_PIG	P26042 sus scrota
6	4	Ξ.			RADI_HUMAN	P35241 homo sapien
10	4	Ξ.		-	RADI_MOUSE	P26043 mus musculu
11	40				RAD1_P1G	P26044 sus scrofa
12	40				BBS2_HUMAN	O9bxc9 homo sapien
13	40	61.5	7	-	BHS2_MOUSE	-
14	C <b>4</b>	61 5		-	RBS2_PAT	Qqqmhq rattus norv
15	39	60.0		٦	COALCLOPE	-
16	3.9	0.09		- 4	Y209_AQUAE	066403 aquifex aec
17	39	C CJ		r i	FTTP4_HTJMAN	PIZORA Nomes Sapility
18	39	0.09		e-	RASO_PYRAR	-
5	38	58.5			INVO_MOUSE:	P48997 mus musculu
20	38	58.5		7	EFER_HUMAN	075154 homo sapien
21	3.7	56.9	m	Т	CHEV_BACSU	_
C1	3.7	4		1	SELD_DICDI	Q94497 dictyosteli
53	3,7	56.9	4	۲-	1:X71_FUSNN	Q8ren3 fusebacteri
24	3.7	56.9		~	SERA_HUMAN	043175 homo sapien
25	3.7	56.9		_	SFRA_PAT	008651 rattus norv
26	47	9,5		-	MOES_MOTISE	P2604] mus musculu
27	37			_	AMT3_CAEEL	Q21565 caenorhabdi
28	3.7	56.0	100	_	RA50_MET.TA	Q58718 methanococ
53			1.4.7		STON_HUMAN	Q13813 home sapien
30	7.5	5.6	C1		SPON_RAT	
31	3.7	56.9	24	_	SPCN_CHICK	P07751 gallus gall
32	36.5	56.2	C) U) U)	_	LUCI_PHOPY	
33	36	55.4	320	Ţ	HLP1_HUMAN	P54257 homo sapien

16   55   55   4   359   1   1   1   1   1   1   1   1   1	P48677 carassius a P47819 ratius norv 193729 ratius norv 193729 ropredo cal 1937248 saccharcmyc 24764 homo sapien 24766 bacillus su p19013 homo sapien 24766 bacillus su p1908 homo sapien 24766 bacillus su p1918 homo sapien 24766 bacillus su p1928 homo sapien 24766 bacillus su p1928 homo sapien 24766 bacillus su p1929 ratius norv 29219 ratius norv 292577 helicobacle car no restrictions on 1929 and the EMBL outstation or restrictions on 1929 and for commercial sapien do for commercial control of the commercial for commercial
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"identification of ezifn as an 81-kDa tyrosine-phosphorylated protein
                                                                                                                                                           SdeD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIJNE-96311348; Pubmed-8713105;
Egerton M., Moritz R.L., broker H., Kelso A., Simpson R.J.;
"Identification of the 70kD heaf shock cognate profeta (HSc70) and
                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metarou; Obordata; Graniata, Vertebrata, Buteleustumi,
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCHI_raxID-9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Offenwaelder B., Obermaier B., Mewes H.-W., Weil B., Wiemann S., Submitted (MAR-2009) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Cytovillin, a microvillar Mr 75,889 protein -cDNA sequence, prokaryctic expression, and chromosomal localization.", J. Biol. Chem. 264-16727-16732(1989)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gould K.L., Bretscher A., Esch F.S., Hunter T., "cDNA cloning and sequencing of the protein tylusine kinase substrate, ezrin, reveals homology to band 4.1.";
                                                                                                                      100.0%; Score 65; DB 1; Length 580;
                                                                                                                                                           Slobul .0
                PHOSPHORYLATION (BY PDGFR)
                                                   PHOSPHORYLATION (BY PDGFR)
                                                                                     BYDERRESCZOOFAA F CRC64;
                                                                                                                                       Pred. No. 0.00071;
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                                                                                                                                                                                                                                                                                                             EZFI.HUMAN STANDAPD: PET; 585 AA. P15411: P24714: Q9NSJ4: Q1-AP90 (Rel. 14, rest sequence update) 01-ANV-1991 (Rel. 20, last sequence update) 15-JUN-2002 (Rel. 41; Last annotation update)
                                  (HY SIMILARITY)
                                                                   (HY SIMILARITY
                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Biol. Chem. 267:19258-19265(1992).
                                                                                                                                                                                                                                                                                                                                                                                                    Ezrin (p81) (Cytovillin) (Villin 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-90076135; PubMed-2591371;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDI.INE-89380299; PubMcd-2674140;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-92406868; PubMed-1382070;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Immunol. 149:1847 1852(1992).
                                                                                   580 AA; 68629 MW;
                                                                                                                                        100.08;
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                                                                                                                                                           Conservative
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                                                 35.3
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                                                                                                                                                                                          1 KEELMLRLQDYEE 1 ₹
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                                                                                                                                        Hest Local Similarity
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57
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Samelson L.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         T cells."
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                                                                                   SEQUENCE
                                                                                                                      Query Match
                MOD_RES
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DOMAIN
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                                                                                                                                                                                entities and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FUNCTION: FROBABLY INVOLVED IN CONNECTIONS OF MAJOR CYTOSKELETAL. STRUCTURES TO THE PLASMA MEMBRANE. SUBCELLULAR LOCATION: MICROVILLAR PERIPHERAL MEMBRANE PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                               TISSUE SPECIFICITY: COMPONENT OF THE MICROVILL OF INTESTINAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 65; DB 1; Length 585; 100.0%; Pred. No. 0.00072;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PHOSPHORYLATION (BY PDGFR). PHOSPHORYLATION (BY PDGFR).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2A844D140E3B06CC CRC64;
                                                                                          PTM: PHOSPHORYLATED BY PROTEIN-TYROSINE KINASES. SIMILARITY: CONTAINS 1 BAND 4.1-LIKE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE: PS00660; BAND 41_1; 1.
PROSITE; PS00661; BAND 41_2; 1.
PROSITE; PS50057; BAND 41_3; 1.
Structural protein, Cytoskeieton; Phosphorylation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAY-1992 (Rel. 22, Created)
01-MAY 1992 (Rel. 22, Last Sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         585 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRUCTURES TO THE PLASMA MEMBRANE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -1- SUBCELLULAR LOCATION: Cytoplasmic.
                                                                                                                                                                                                                                                                          EMBL: J05021; AAA61278.1; ALT_INIT.
EMBL: AL162086; CAB82418.1: ALT_INIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ezrin (p81) (Cytovillin) (Villin 2).
                                                                                                                                                                                                                                                                                                                                                                                                futerFlo, iPRÖÖÖ798, Ezzrad/moesin.
Pfam; PF00373; Band_41; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Fig.
                                                                                                                                                                                                                                                                                                                                                                                 InterPro: IPR000299; Band_4.1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            69267 MW;
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                                                                                                                                                                                                                                                            EMBL; X51521; CAA35893.1;
EMBL; J05021; AAA61278.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                         PRINTS; PR00935; BAND41.
SMART; SM00295; B41; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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                                                                                                                                                                                                                                                                                                                                                   HGNC:12691; VIL2.
                                               (CYTOPLASMIC SIDE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              343 KEELMLRLQDYEE 355
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                                                                          EPITHELIAL CELLS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                       PIR; S09263; S09263.
PIR; A34400; A34400.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           585 AA;
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es 13, Conserv
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MOD_RES
CONFLICT
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A protein related to encaryal and becterial DNA-motor proteins in the hyperthermophilic archaeun Sulfolobus acidocaldarius.";

PUNCTINOL 45:107-114 (1997).

PUNCTION INVOLVED TO BASES SIGNIFIES STRANG ELEGAL (USAF). The rad50/more to complex possesses signale strand endomotease activity and ATP-dependent deather strand-specific exonuclease activity. Rad50 provides an ATP-dependent control of mrell by unwinding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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-!- TISSUE SPECIFICITY: COMPONENT OF THE MICROVILLI OF INTESTINAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     repositioning DNA ends into the mrell active site (By
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SUBUNIT: Forms a complex with mrell (By similarity).
SIMILARITY: BELONGS TO THE SMC FAMILY. RAD50 SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length, 585,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 62, DB 1, Lengtl. SBS.
Pred No. 0.0024;
                                                                                                                                                                                                                                                                                                                                                                                                                                                PHOSPHORYLATION (BY PDGFR)
                                                                                                                                                                                                                                                                                                                                                                                                                    PHOSPHORYLATION (BY PDGFR) (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                              (BY SIMILARITY).
2057EDE2P2BOD5D2 @PG64,
            EPITHELIAL CELLS.
PTM: PHOSPHORYLATED BY PROTEIN-TYROSINE KINASES.
SIMILARITY: CONTAINS 1 HAND 4.1-LIKE DOMAIN.
                                                                                                                                                                                                                                                                                                          SMART, SM00295, B41, 1.
PROSTTE, PS00660, BAND 41_1, 1.
PROSTIE: PS00661, BAND 41_2; 1.
PROSTIE: PS50667; BAND 41_3: 1.
Structural protein; Cytoskeleton; Phosphorylation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA double-strand break repair rad50 ATPase.
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BAND 4.1-LIKE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIRAIN AIGC 33909 / MOIB 11770 / USM 639,
MEDLINE-97362314: Pubmed-9211741;
                                                                                                                                                                                                      PIR: B41129; B41129.

MACD: MG1-88937; V1122.

InterPro: IPR000299; E2/rad/moesin.
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                                                                                                                                                                                        EMBL; X60671; CAA43086 1;
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343 KERLMLRLQDYRQ 355
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or send an email to licenselisb'sib.ch).
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or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gabs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Actinopterygii, Neupterygii, Teleostei, Ostariophysi, Cypriniformes, Cyprinidae, Danio.
NCBL_TaxID=7955;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota: Metazoa; Chordata; Craniata; Verfebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Match 67.7%; Score 44; DB 1; Length 886; Local Similarity 66.7%; Pred. No. 5.2;
                                                                                                                                                                                                                                                                                                                                                                                       Property, Programmer 1.

Probom: PRO0465; SMC_N: 1.

Probom: PRO06065; ABC_Lransportr; 1.

DNA .epair. Hydrolase: AIP-binding; Coiled coil.

NP BIND 37 ATP (BY SMILARITY).

TYA 727 COILED COIL (FOTENTIAL).

TYA 727 COILED COIL (FOTENTIAL).
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SEQUENCE: 715 AA; 79125 MW; 326770AC45836C90 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ..ast sequence update)
..ast annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Brachydanio rerio (Zebrafish) (Danio rerio).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bardet Biedl syndrome 2 protein homolog.
                                                                                                                                                                                                                                                                                                                                                              InterPro; (PRG03439; ABC_transportr.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-21181710; FubMed-11285252;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bardet-Biedl syndrome (BBS2).";
Hum. Mol. Genet. 10:865-874(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15-JUN-2002 (Rel. 41, Created)
15 JUN-2002 (Rel. 41, Last sequents-JUN 2002 (Rel. 41, Last annomalis-JUN 2002 (Rel. 41, Last annomalis-JUN 2003 (Rel. 41, Last annomalis-JUN 2003 (Rel. 41, Last annomalis-JUN 2003 (Rel. 41)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  56.2%;
61.5%;
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Best Local Similarity 61.5%,
Best as 8, conservative
                                                                                                                                                                                                                                                                                                                        EMBL: Y10687; CAA71688.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               345 KONLMLELKNYEE 357
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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1 KEELMLRLODYEE 13

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Mond V. Gwilliam R., Rajandram M.A., Lyne M., Lyne R., Stewart A.,
Mond V., Gwilliam R., Rajandram M.A., Lyne M., Lyne R., Stewart A.,
Squiros J., Peat N., Hayles T., Raker S., Easham F., Rewmin S.,
RA Brown D., Brown S., Chilliamworth T., Churcher C.M.,
A Collins M., Cohnor R., Cromin A., Davis P., Fettwell T., Frascr A.,
Collins M., Cohle A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
A Holroyd S., Horney P., Mungall K., Hurphy L., Niblett D., Odell C.,
A James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
Money P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
A Jaylor K., Sammods M., Squares R., Squares S., Stevens K.,
A Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
A skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
A skelton J., Volckaert G., Act. R., Robben J., Grymonprez B.,
Woodward J., Volckaert G., Act. R., Robben J., Grymonprez B.,
A skelton J., Volckaert G., Act. R., Robben J., Grymonprez B.,
A skelton J., Volckaert G., Act. R., Robben J., Grymonprez B.,
A skelton J., Volckaert G., Act. R., Robben J., Grymonprez B.,
A skelton J., Volckaert G., Act. R., Robben J., Grymonprez B.,
A skelton J., Volckaert G., Act. R., Robben J., Grymonprez B.,
A skelton J., Volckaert G., Act. R., Robben J., Grymonprez B.,
A skelton J., Volckaert G., Act. R., Robben J.,
A short R., Taylor K., Salalardin C., Tallada V.A., Garzon A., Thode G.,
A lalibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
A dalibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
A dalibert B., Drawer S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
A dalibert G.V., Act. R., Robben J., Sanchez, M., del R., P. Benito J.,
A Shpakovski G.V., Usery D., Barrell B.G., Nurse P.,
A Shpakovski G.V., Usery D., Barrell B.G., Nurse P.,
A Shpakovski G.V., Usery D., Barrell B.G., Nurse P.,
A Shpakovski B. S., Relace B., Moore Bequence Sequence S., Sanchez B., Sanchez B., Sanchez B., Sanchez B.,
A Shpakovski G.V., Usery D., Barrell B.G., Nurse P.,
A Shpakovski B., Sanchez B., Sanchez B., Sanc
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the Biroppan Bioinformatics institute. There are no restrictions on its
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modified and this statement is not removed. These by and for commercial
entities requires a license agreement. (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1. PATHWAY: PHOSPHOLIPID BLOSYNTHESIS; CDP-ETHANOLAMINE SYNTHESIS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        :!- CATALYIIC ACTIVITY: CIP + ethanolamine phosphate - diphosphate
                                                                                                                    16-oCT-2001 (Rel. 40, Last sequence update)
15-oDN-2002 (Rel. 41, Last annotation update)
15-oDN-2002 (Rel. 41, Last annotation update)
16-oDN-2012 (Rel. 41, Last phosphate cytidylyltransferase (EC 2.7.7.14)
(Phosphorylethanolamine transferase) (CIP:phosphorthanolamine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPRO04821; Cyttran_rei;
InterPro; IPR004820; Cytidylyltransi.
PIGMEAMS; TIGR00125; Cyt_tran_rel; 2.
Infansierase, Nucleotidyltransferase; Phosphoijpid biosynthesis
DOMAIN 1 182 CAFALVIIC (POTENITAL).
SEQUENCE 365 AA: A1566 WW: ACHMEAG74AHH4734 CPC44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- SIMILARITY: BELONGS TO THE CYTIDYLYLTRANSFERASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ouery Match 63.1%; Score 41; DB 1; Length 365;
Bost Local Similarity 61.5%; Pred. No. 6.6;
                                                                                                                                                                                                                                                                                                                                      Eukaryota; Panqi; Asromycota; Schimosaccharomycetes;
Schimosaccharomycetales; Schimosaccharomycetaceae;
                                365 AA.
                                                                                                                                                                                                                                                                                                         Schizosaccharomycos pombo (Pission yeast)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               or send an email to licensewisb-sib.ch).
                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIJINE-21848401; PubMcd-11859360;
                                                                                       16-off-2001 (Rel. 40, Created)
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                                STANDARD;
                                                                                                                                                                                                                                                  cytidylyltransterase)
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                                                                                                                                                                                                                                                                                                                                                                                                       Schizosaccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID-4896;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SECOND STEP.
                                                                                                                                                                                                                                                                            SPAC15E1.05C.
                                ECT1_SCHPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-972;
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                                                          .91TU90
ECT1_SCHPO
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-1- DATABASE: NAME-Atlas Genet. Cytogenet. Oncol. Haematol.; WWW-"http://www.infobiogen.fr/services/chromcancer/Genes/MSNID363.html"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a coliaboration between the Swiss institute of Bloinformatics and the PMH, outstation the European Bloinformatics institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/ammonnecfor sond an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Moesin: a member of the protein 4.1-talin-errin family of proteins."; Proc. Natl. Acad. Sci. U.S.A. 88:8297-8301(1991).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -1- FUNCTION: PROBABLY INVOLVED IN CONNECTIONS OF MAJOR CYTOSKELETAL STRUCTURES TO THE PLASMA MEMBRANE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -1- TISSUE SPECIFICITY: IN ALL TISSUES AND CULTURED CELLS STUDIED.
-1- SIMILARITY: CONTAINS I BAND 4 1-LIKE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                 Eukaryola, Metazoa, Chordata, Craniata, Verrebrata, Euteleostomi,
Mammalia: Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ر
ت
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A., AND SEQUENCE OF 1:15; 53-59 AND 413-434
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tipe. 1; Mismatches 3; indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Howden P.;
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BAND 4.1-LIKE.
; 96CE7C28D55A8176 CRC64;
                                                                                                                                                                                                01-MAY-1962 (Rel. 22, created)
01-AUG-1992 (Rel. 23, Last sequence update)
15-JUN 2062 (Rel. 41, Last annotation apdate)
Mocsin (Mcmbianc organizing extension spike protein).
                                                                                                                                              FRT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE-Placenta;
MEDLINE-SIGLO840; PubMed-1924289;
Lankes W.T., Furthmayr B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE: PS00660; BAND_41_1; 1.
PROSITE: PS00661; BAND_41_2; 1.
PROSITE: PS50057; BAND_41_3; 1.
Structural protein: Cytoskeleton.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Aarhus/Ghent-20PAGE: 3515; IEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR000299; Band_4.1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         67689 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL, M59066; AAA36322.1; -.
EMBL, 298946, CAB46379.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00373; Band_41; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Senserratire
                                                                                                                                                 STANDARD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRINTS; PR00935; BAND41.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      333 KORVMLRROHYEE 345
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Genew; HGNC:7373; MSN.
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                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (Human).
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Hest Local Similarity
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                                                                                                                                                 MORS_HUMAN
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                                                                                                                                                                                                                                                                                                                                                  Lankes W.T., Schwartz-Albiez R., Furthmayr H.;
"Clonding and sequencing of porcine moesin and radixin cDNA and
identification of highly conserved domains.";
Hophys, Acta 1216:479-482(1993)
-!- FUNCTION: PROBABLY INVOLVED IN CONNECTIONS OF MAJOR CYLOSKELETAL.
STRUCTURES TO THE PLASMA MEMBRANE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota, Motazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia; Eutheria; Primates, Catarrhini, Hominidae; Humo.
                                                                                                                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebruta, Euteleostomi;
Mammalia; Eutheria; Cetartlodactyla, Suina; Suidae; Sus.
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                                                                                                                 01-AUG-1992 (Pel 24, Last sequence opdate)
16-OCT-2001 (Rel. 40, Last annotation opdate)
Mocsin (Membrane-organizing extension spike protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIMILARITY: CONTAINS 1 BAND 4 1-LIKE DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-FEB-1994 (Rel. 28, Created)
01-FFB-1994 (Rel. 28, Last sequence update)
16-OCT 2001 (Rel. 40, Last annotation update)
                                                         576 AA
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BAND 4.1 LIKE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              E2/rad/moesin
                                                                                                                                                                                                                                                                                                                                MEDI.INE+94092743; PubMcd-8268231;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Structural protein; Cytoskeleton.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE, PS00660: BAND 41_1; 1. PROSITE; PS00661; RAND 41_2; 1 PROSITE; PS50057; BAND 41_3; 1.
                                                                                           01-MAY-1992 (Rel. 22, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR000299; Band_4.1.
InterPro; IPR000798; Ez/rad/mo
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Matches 9, Conservative
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Pfam; PF00769; ERM; 1.
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                                                       STANDARD;
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                                                                                                                                                                                                          Sus scrofa (Pig).
                                                                                                                                                                                                                                                           NCBI_TaxID-9823;
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                                                       MOES_PIG
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                                 MOES_PIG
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"Padrixin is a novel member of the band 4.1 lamily.";
"Todil Hiol. 115:1039-1048(1991).
--- FUNCTION: PROBABLY PLAYS A CHUCIAL MOLE HE HINDING OF THE
HARBDE BUD OF ACTIN FILAMENTS TO THE PLASMA MEMBRANE.
--- SUBGEDLULAR LOCATION HIGHLY CONCENTRATED IN THE UNDERCOAT OF THE
CELL-TO-CELL ADHERENS JUNCTION AND THE CLEAVAGE FURROW IN THE
                                                                                                                                                                                  Genomics 16:199-206(1993).
-!- FUNCTION: PROBBELY PLAYS A CRUCIAL ROLE IN THE BINDING OF THE BARBED END OF ACTIN FILAMENTS TO THE PLASMA MEMBRANE.
-!- SUBCELLULAR LOCATION HIGHLY CONCENTRATED IN THE UNDERGOAL OF THE CELL-TO-CELL ADHERENS JUNCTION AND THE CLEAVAGE FURROW IN THE
IISSUE-Liver;
MEDIZE 932378, Fulked-8486377;
MEDIZE 932378, Fulked-8486377;
Milgenbus K.K., Milatovich A., Francko U., Furthmayr H.;
"Molecular cloning, cDNA sequence, and chromosomal assignment of the human tadixin gate and two dispersed pseudogenes.";
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Mammalia, Eutheria, Rodentia, Sciurognathi: Muridae, Murinae, Mus.
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DOMAIN 58 225 BAND 4.1-LIKE.
DOMAIN 470 477 POLY-PRO.
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                                                                                                                                                                                                                                                                                                                                                                                 INTERPHASE AND MITOTIC PHASE, RESPECTIVELY.
-!- SIMILARIIY: CONTAINS 1 BAND 4.1-LIKE DOMAIN.
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01-MAY-1992 (Bel. 22, Last sequence update)
1b-001-2001 (Rel. 40, Last annotation update)
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Intelbe; Propo@788; Ez7rad/mocsin.
Pram: PPO@778; Hand_41: 1.
Pram: PPO@769; EPM: 1.
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Aarnus/Ghent-LDPAGE; 2501; IEF.
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SMART; SM00295; B41; 1.
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MIM: 179410; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-94092743; Febbred 8268241; Jankes W.L. Schwartz-Albice R., Furthmayr H.; Febbred S. C., Schwartz-Albice R., Furthmayr H.; Febbred and sequencing of porcine meests and radixin come and identification of highly conserved domains."; Biochim. Biophys. Acta 1216:479-482(1993).

11- FUNCTION: PROBABLY PLAYS ACRGIAL ROLE IN THE BINDING OF THE BARBED END OF ACTIN FILAMENTS TO THE PLASMA MEMBRANE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUBCELLULAR LOCALLON: HIGHLY CONCENTRATED IN THE UNDERCOAT OF CELL TO CELL ADHERENS JUNCTION AND THE CLEAVAGE FURROM IN THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Structural protein; Cyroskeleton; Actin-binding; Capping protein, DAMAIN 58 225 BAND 4.1-LIKE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Enkaryota, Metazea: Cherdata, Cramiata, Vertebrata, Euteleostomi,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61.5%; Score 40: DB 1: Length 583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3; indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mammalia: Eutheria: Cetartiodactyla; Suina; Suidae; Sus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3219A52ECDCB7ERE CPC64;
INTERPHASE AND MITGHE PHASE, RESPECTIVELY.
SIMILARITY: CONTAINS 1 HAND 4.1-LIKE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INTERPHASE AND MITGLE PHASE, RESPECTIVELY. SIMILARITY: CONTAINS 1 BAND 4.1-LIKE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAY-1992 (Rel. 22, Greated)
01-MAY-1992 (Rel. 22, Lust sequence update)
16-OCT 2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             POLY-PRO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No.
                                                                                                                                                                                                                                                                                                       MGD; MG1:97887; Rdx.
InterPro: IPR000299; Band_4.1.
InterPro: IPR000799; Ez/rad/moesin.
Plam: PF00174; Band_41; 1.
Ptam: PF00769; EKM: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS00660; BAND_41_1; 1. PROSITE; PS00661; BAND_41_2; 1. PROSITE; PS50057; BAND_41_3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SR3 AA. 68451 MW.
                                                                                                                                                                                                                                                             EMBL; X60672; CAA43087.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMHL; M86444; AABU2865.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rest Local Similarity 69.28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                              PRINTS; PR00935; BAND41.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               477
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 KEELMLRLQDYEE 13
                                                                                                                                                                                                                                                                                      PIR; A41129; A41129.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       SM00295; B41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Radixin (Moesin B).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RADI_PIG
P26044;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    SMART;
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MEDLINE 21181710; Furbred 12.85.55;
Nishimura D Y., Searby C.C., Carmi R., Elbedour K., Van Maldergem L., Fulton A.B., Lam B.L., Powell B.R., Swiderski R.E., Budge K.E., Heider N.B., Kwiltek-Black A.E., Ying L., Dubl D.M., Gorman S.M., Heon E., Lannaccone A., Bonneau D., Hiesecker L.G., Jacobson S.G., Stone E.M., Shellield V.C.;
"Positional cloning of a novel gene on chromosome 16q causing Bardet-Black Conet. 10:865 874(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
ISOGALT, OLD T., Hayashi K., Suqiyama T., Otsuki T., Suzuki Y.,
ISOGAL T., Otda T., Hayashi K., Suqano S., Shiratori A., Sudo H.,
Nishikawa T., Naqai K., Suqano S., Shiratori A., Sudo H.,
Mayatsuma M., Hosoiti T., Kaku Y., Kodaira H., Kondo H., Suqawara M.,
Takabiashi M., Chika Y., Ishida S., Murakama K., Guo Y., Takiyuchi S.,
Watanabe S., Kimara K., Marakami K., Ishida S., Marakami K., Saito K.,
Yamamoto J., Wakamatsu A., Nakamura Y., Nagahati K., Masuho Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VARIANTS HBSZ S-70; A-104; Q-315; W-315; I-558 AND P-632. MEDLINE-21451214; PubMed-11567139; Ratisanis N., Ansley S.J., Badano J.L., Eichers E.K., Lewis K.A., Hoskins B E, Scambler P I, Pavidson W S., Reales P.L., Lupski J.R.; Prallelle inheritance in Bardet-Biedl syndrome, a mendelian recessive disorder.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                     Structural protein; Cytoskeleton; Actin-binding; Capping protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N A , VAPIANT BBS2 GLY-75, AND VARIANT VAL(123.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 40; DB 1; Length 583;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3; indels
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"NEDG human cDNA sequencing project.";
Submitted (MAY-2001) to the EMBL/Genbank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                  59AEA286DCAF7397 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        09BXC9; 096CM0; 096SN9;
15-JUN-2002 (Rel. 41, Greated)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last amoctation update)
                                                                                                                                                                                                                                                                                                                                            BAND 4.1-LIKE, POLY-PRO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No.
                          InterPro; IPR000299; Band_4.1.
InterPro; IPR000798; Ez/rad/moesin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-JUN-2002 (Rel. 41, Last annota
Bardet-Biedl syndrome 2 protein.
                                                                                                                                                                                                                 PROSITE: PS00660; HAND-41_1; 1.
PRISITE: PS00661; BAND-41_2; 1.
PROSITE: PS50057; BAND_41_4; 1.
                                                                                                                                                                                                                                                                                                                                                                                                               68549 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               69.28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61.5%;
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                                                                                         Ptam: PF00373; Band_41: 1.
Ptam: PF00769; ERM: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 69.27
Matches 9; Conservative
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                                                                                                                                                     PRINTS; PR00935; BAND41.
                                                                                                                                                                                                                                                                                                                                                   225
                                                                                                                                                                                          SMART; SM00295; B41; 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     344 KEELMERLRQIEE 356
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (Human)
PIR; S39805; S39805.
                                                                                                                                                                                                                                                                                                                                                                                                        583 AA;
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                                                                                                                                                                                                                                                                                                                                                   58
470
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                                                                                                                                                                                                                                                                                                                                                                                                                  SHOURNCE
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           type 2 (BBS2). Burdet Biedl syndrome (BBS) is a genetically heterogeneous, autosomal recessive disorder characterized by Asally, severe pinacutary retineathy early once, descit, polydactyly, hypogenitalism, renal malformation and mental retardation. Secondary features include diabetes mellitus, hypertension and conjenital heart disease. A relatively high incidence of BRS is found in the mixed Arab populations of Kuwait and in Bedomin tribes throughout the Middle East, most likely due to the high rate of consaguinity in these populations and a
                                                                                                                                                                                                                                                                                                                                                                                                                       N -> S (IN BBS2).
/FTIG-VAR_01316.
V -> G (IN BRS2; IN LINKAGE
DISEQUILIBRIUM WITH VAL-123 IN A BEDGUIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /FIId-VAR 013164
1 -> V (IN EINRACE DISEQUILIBRIUM WITH
GLY-75 IN A BEDOUIN KINDRED).
DISEASE: Defects in BBS2 are the cause of Bardet Biedl syndrome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus (Mouse).
Enbarrata - Madazaa, Chatdata, Charlata, Vertebrata, Puteleestomi,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0
                                                                                                                                                                                                                                                                                                                                                                                                        Disease mutation; Bardet Biedl syndrome; Obesity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61.5%; Score 40: PB 1; length 721; 53.8%; Pred. No. 21;
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A > V (IN REF. 3).
C - S (IN REF. 3).
C - S (IN REF. 2).
Y -> H (IN PFF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /FTId=VAR_013165.
R -> Q (TN PP...
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-> A (IN BBS2).
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E. . F. (IN PBS2).
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15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Bardet-Biedl syndrome 2 protein homolog.
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/FTId-VAR_013166
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FTIG-VAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /FTIG-VAR_CE -> G (IN
                                                                                                                                                                                                                                                                                                            EMBE, AF342736, AAK28652.1;
EMBE, AK027635; BAB55252.1; -.
EMBE, BC014140- AAH14140 1: -
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09CWF6;
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                                                                                                                                                                                                                                                                                                                                                                                                               A Arakawa T., Harra A., Shihada K., Yoshino M., Itoh M., Ishii Y., A Arakawa T., Harra A., Shihada K., Yoshino M., Itoh M., Ishii Y., A Arakawa T., Harra A., Fukunishi Y., Konno H., Adachi J., Fukuda S., Asaraaka I., Salico T., Ckaraki Y., Gojobori T., Bonc H., Kasukawa T., Salico R., Asaraaka I., A Salico T., Ckaraki Y., Gojobori T., Bonc H., Kasukawa T., Salico R., Asaraaka I., A Fleischmann W., Gaastorland T., Gissi C., King R., Kochiwa H., A Fleischmann W., Gaastorland T., Gissi C., King R., Kochiwa H., A Schriml L.M., Staubli F., Suzuki K., Tomita M., Wagner L., Washio I., Asakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Dakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., A Brake T., Bellell D., Bojunga N., Carninci P., de Bonaldo M.F., A Brake T., Bull D., Hoffmann M., Hume D.A., Kamiya M., Lee N.H., A Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., Androhe P., Ring H., Ringwald M., Rodriguez I., Sakamoto N., Sasaki H., Zoye-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L., A Wishiawa K., Shopenbach K., Rawaji H., Kohtsuki S., Anavashiraki V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          entities requires a incurse squeezent (See http://www.isb sib.ch/announce) or send an email to licensewisb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SHED
                                                                                         STRAIN-Swiss Webster / NIH, TISSUE-Fetal;
MISDLINE-218179, Debacd-1128252.
Misbline-218179, Debacd-1128252.
Misbline-16-N., Scarby C.C., Calmi R., Eibedout K., Van Maidergem L. Fulton A.R., Lam H.L., Powell B.R., Swiderski R.E., Hugge K.E., Fulton A.R., Lam H.L., Powell B.R., Swiderski R.E., Hugge K.E., Hadader M.R., Mischell B.R., Swiderski R.E., Tannaccone A., Ronneau D., Blesseker L.G., Jacobson S.G., Stone R.M., Sheffield V.C., Ronneau D., Blesseker L.G., Jacobson S.G., Byestitonal cloning of a nevel gene on chromosome 16g causing Bartach Beat act. Bical syndsone (1882).
  Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Functional annotation of a full length mouse cONA collection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61.5%; Score 40; DB 1; Length 721; 53.8%; Pred. No. 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2. Indela
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          79931 MW; GGILPAB7834B614F4 CPC64;
                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN-1774L,56:1 IISSUF-Embsyonic stem cells;
Madrink Fro85666; PathMcd-11217851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Bardet Biedl syndrome 2 protein homolog.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       721 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4, Mishatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FRT:
                                                                                                                                                                                                                                                                                 Bardet Biedl syndröme (BBS2).";
Him Moi Genet 10:865-874(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AF342737; AAK28553.1; -. EMBL; AK010779; BAB27176.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                53.885
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nature 409-685-690(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 53.8
Matches 7, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MCI:2135267; Bbs2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  345 KONLILELRNYEE 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 KEELMLRLQDYEE 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7.11 AA:
                                                                   SELTENTE FROM N.A.
                        NCB1_1axiD 10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hayashiraki Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SECTENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BBS2_FAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               099MH9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 14
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the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See http://www.isb-sib.ch/announce/
or sound an email to license*isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          this SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                             Nishimura D.Y., Searby C.C., Carmi R., Elbedour K., Van Maldergem L., Fullon A.B., Lam B.L., Powell B.R., Swiderski R.E., Bugge K.E., Haider N.B., Kwitek-Black A.E., Ying L., Puhl D.M., Gorman S.M., Heon E., Tannackone A., Bunneau D., Biesecker E.G., Javobson S.G., Stone E.M., Sheffield V.C., "Positional Coning of a novel gene on chromosome 16g causing Bandel Bledl syndrome (BRS).":
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Caps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FUNCTION: Catalyzes the phosphorylation of the 3'-hydroxyl group of dephosphoroenzyme A to form occuryme A (By similarity). CATALYTIC ACTIVITY: Alephospho-CoA = Aub + CoA. PATHWAY: Coenzyme A (YoA) blosynthesis; Litth (Last) step. STRUCELLULAR LOCATION: Cyloplasmic (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Shimizu T., Obtani K., Hirakawa H., Obshima K., Yamashita A., Shiba T., Oqasawara N., Hattori M., Kubara S., Hayashi H., "Complete genome sequence of Clostridium pertringens, an anaerobic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     [5-JUN-2002 (Rel. 4), Created)
15-JUN-2002 (Rel. 4), Last sequence update)
15-JUN-2002 (Rel. 4), Last annotation update)
16-JUN-2002 (Rel. 4), Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Manteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61.5%; Score 40; DB 1; Length 721; 54.8%; Pred. No. 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2; indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIMILARITY: Belongs to the coaE tamily
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                STRAIN-Sprague-Dawley;
MEDLINE-21181710; PubMed-11285252;
                                                                                                                                                                                                                                                                                                                                                                         Bardet Biedl syndrome (BBS2).";
Hum. Mol. Genet. 10:865-874(2001).
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Matches 7: Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Clostridium pertringens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 KEELMLRLQDYEE 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-13 / Type A;
                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
NCB1_TaxID-10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCB1_Tax1D-1502;
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EMBL; AP003192; BAB81699.1; -. Interpro; IPR001977: Depp\_CoAkinase.

The state of the s

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0; Gaps
                                                                                      Transferase, Kinase, ATP-binding, Coenzyme A biosynthesis;
                                                                                                                                                                                          60.0%; Score 39; DB 1; Length 199; 45.2%; Pred, No. 7.7;
                                                                                                                                                                                                                                   1; Indels
                                                                                                                             ATP (POTENTIAL).
797F5841372C363C CRC64;
                                                                                                                                                                                                                                   6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                            Search completed: January 16, 2903, 16:51:12
Job time : 20.9429 secs
Plam; PF01121; CoaE: 1.
ProDom; PD003329; Depp_CoAkinase; 1.
TiGKFAMS; TIGR00152; UPF0038; 1.
                                                                 PROSITE; PS01294; COAE; FALSE_NEG.
                                                                                                                                               199 AA; 23152 MW:
                                                                                                                                                                                                           Similarity 46.2%;
6; Conservative
                                                                                                                             15
                                                                                                                                                                                                                                                                                                                 92 KEELEIKLKEYEK 104
                                                                                                                                                                                                                                                                        1 KEELMLRLQDYEE 13
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